S3 Table. Association between a binary affinity classification based on predicted $\Delta\Delta G$ with high- and low- binding RBD binding ACE2 variants identified by deep mutagenesis.

mCSM-PPI2	0 02		recal. mCSM-PPI2	nCoV-S High sorts log ₂ enrichment ratio	
(kcal mol ⁻¹)			(kcal mol ⁻¹)		
	< 0	>= 0		< 0	>= 0
< 0	304	72	< 0	235	41
>= 0	47	14	>= 0	116	45
$\chi^2 = 0.27$, p = 0.6				$\chi^2 = 10$, p = 0.001	